REMARKS

Restriction has been required between what the PTO deems to be four patentably distinct inventions, namely:

Group I, comprising claims 1-7 and 20 and drawn to a polypeptide capable of modulating the autoimmune response of an individual to acetylcholine receptor and pharmaceutical compositions comprising the same;

Group II, comprising claims 8-19 drawn to a method of producing a polypeptide comprising a DNA molecule, vectors, and cells comprising the same; and

Group III, comprising claim 21 and drawn to a method for alleviating and/or treating myasthenia gravis; and

Group IV, comprising claim 22 and drawn to a method for diagnosing myasthenia gravis.

Applicants elect Group II comprising claims 8-19 for prosecution on the merits.

The examiner further requires restriction to one of the sequences SEQ ID NOs:1, 2, 5, 6, 7 and 8.

Applicants provisionally elect SEQ ID NO:2, that is a DNA molecule encoding a polypeptide of SEQ ID NO:2, with traverse.

The reason for traversal is that SEQ ID NOs:1, 5, and 7 are nucleotide sequences which encode the amino acid

sequences SEQ ID NOs:2, 6, and 8, respectively. Therefore, at least SEQ ID NO:1 which encodes for the amino acid sequence SEQ ID NO:2 should be examined together with SEQ ID NO:2. Furthermore, as disclosed on pages 8 and 9 of the specification, the sequence are structurally and functionally similar. For example, SEQ ID NO:2 is residues 1-210 of the human acetylcholine receptor (hAChR) α-subunit, SEQ ID NO:6 is residues 1-210 of hAChR α-subunit but with a sequence of 25 residues encoded by the p3A exon of hAChR α-subunit inserted between residues 58 and 59, and SEQ ID NO:8 is residues 1-205 of hAChR α-subunit but with a sequence of 25 residues encoded by the p3A exon of hAChR α-subunit inserted between residues 58 and 59. Thus, the only difference between SEQ ID NO:6 and SEQ ID NO:8 is an extra five residues at the C-terminal end of SEQ ID NO:8 and the only difference between SEQ ID NO:2 and SEQ ID NO:6 is the 25 residue insertion between residues 58 and 59.

As the nucleotide sequences SEQ ID NOs:1, 5 and 7 encode amino acid sequences SEQ ID NOs:2, 6 and 8, they are also structurally and functionally related. Accordingly, each sequence does not require a separate search of the literature.

Withdrawal of the restriction requirement with regard to SEQ ID NOs:1, 2, 5, 6, 7 and 8 and examination of all SEQ ID NOs:1, 2, 5, 6, 7 and 8 are therefore respectfully requested.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with markings to show changes made".

Respectfully submitted,

BROWDY AND NEIMARK, P.L.L.C.
Attorneys for Applicant(s)

By _____
Allen C. Yun
Registration No. 37,971

ACY:wlm
Telephone No.: (202) 628-5197
Facsimile No.: (202) 737-3528
G:\BN\Y\YEDA\fuchs2A\pto\Amendment Resp to RR.doc

Version with Markings to Show Changes Made

In the Claims

Claim 8 has been amended as follows:

8 (Amended). A DNA molecule coding for ~~the~~ a polypeptide ~~according to claim 1~~ capable of modulating the autoimmune response of an individual to acetylcholine receptor, said polypeptide being selected from the group consisting of:

(i) a polypeptide consisting of the amino acid sequence of SEQ ID NO:6;

(ii) a polypeptide consisting of the amino acid sequence of SEQ ID NO:8;

(iii) a polypeptide corresponding to amino acid residues 1-121 of SEQ ID NO:2;

(iv) a polypeptide corresponding to amino acid residues 1-146 of SEQ ID NO:6;

(v) a polypeptide corresponding to amino acid residues 122-210 of SEQ ID NO:2;

(vi) a polypeptide as in (i) to (v) or the polypeptide Hα1-210 of SEQ ID NO:2 in which one or more amino acid residues have been added, deleted or substituted by other amino acid residues in a manner that the resulting polypeptide is capable of suppressing experimental myasthenia gravis in animal models;

(vii) a fragment of a polypeptide as in (i) to (vi), which fragment is capable of suppressing experimental myasthenia gravis in animal models;

(viii) a polypeptide comprising two or more fragments as in (vii) fused together with or without a spacer;

(ix) a polypeptide, or a fragment as defined in (i)-(viii), or the polypeptide Hα1-210 of SEQ ID NO:2, fused to an additional polypeptide at its N- and/or C-termini; and

(x) soluble forms, denatured forms, chemical derivatives and salts of a polypeptide or a fragment as defined in (i)-(ix).